

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: January 16, 2003, 16:39:12 - Search time 7:28:571 seconds
(without alignments)
28 464 Million cells updated/acc

Title: US-09-856-070-26
Perfect score: 28
Sequence: 1 QDYEE 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 4176328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	252	1 QPC6_HUMAN	Q9566 homo sapien
2	28	100.0	262	1 QPC6_MOUSE	Q9418 mus muscu
3	28	100.0	338	1 PAHX_HUMAN	G1482 homo sapien
4	28	100.0	385	1 SWY_PYRAH	Q9071 pyrococcus
5	28	100.0	505	1 SYE_CHLEN	Q9223 chlamydia p
6	28	100.0	540	1 EERI_HUMAN	P1676 bos taurus
7	28	100.0	585	1 EERI_HUMAN	P1531 homo sapien
8	28	100.0	624	1 USK1_CYLFU	Q1943 cylinthre
9	28	100.0	911	1 SWO_SCHRO	Q9728 schizosac
10	28	100.0	824	1 DQ20_HUMAN	Q9016 homo sapien
11	28	100.0	875	1 E22_MOUSE	Q6334 mus muscu
12	28	100.0	1332	1 KAP_HUMAN	Q95163 homo sapien
13	25	89.3	82	1 Y070_METJA	Q60373 methanococ
14	25	89.3	130	1 CAL2_MOUSE	Q9903 mus muscu
15	25	89.3	134	1 CAL2_RAT	P13033 ratu
16	25	89.3	141	1 VC36_HARTN	P4230 haemophilu
17	25	89.3	168	1 RFP3_TOBAC	Q03683 nicotiana
18	25	89.3	187	1 RFP_MYCLE	Q9080 mycobacteri
19	25	89.3	187	1 EEP_MYCTJ	Q95019 mycobacteri
20	25	89.3	203	1 E2CC_DROME	P24156 drosophila
21	25	89.3	212	1 LIPB_HABIN	P44464 haemophilu
22	25	89.3	239	1 THB3_ANEPH	P33632 anemia phyl
23	25	89.3	258	1 L231_HUMAN	Q75822 homo sapien
24	25	89.3	263	1 Y225_METJA	Q57678 methanococ
25	25	89.3	280	1 EYF2_MOUSE	P42280 drosophila
26	25	89.3	289	1 CMFN_SCHPO	Q9076 schizosacch
27	25	89.3	290	1 R1P1_TOHAC	Q03681 nicotiana t
28	25	89.3	292	1 R1P2_TOHAC	Q03682 nicotiana t
29	25	89.3	293	1 R1P8_TOHAC	Q03686 nicotiana t
30	25	89.3	298	1 C1E_HUMAN	P29774 homo sapien
31	25	89.3	299	1 C1F_BOVIN	P19879 bos taurus
32	25	89.3	315	1 GAW_YEAST	P50085 saccharomye
33	25	89.3	339	1 V021_YEAST	P53352 saccharomye

RESULT 1
ORC6_HUMAN
ID ORC6_HUMAN STANDARD: PRT: 252 AA.
AC Q9V5N6;
DT 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
UI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Origin recognition complex subunit 6.
GN ORC6L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_taxonomy:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dean F.B., O'Donnell M.
RT cDNA clone of a human for Saccharomyces cerevisiae derived from Homo sapiens.
RL Submitted (MAP-1999) to the EMBL/GenBank/Trna databases.
CC 1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO THE APS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN ATP-DEPENDENT MANNER.
CC 2- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS.
CC 3- SUBCELLULAR LOCATION: Nuclear.
CC 4- SIMILARITY: BELONGS TO THE ORC6 FAMILY.
CC THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.ebi.ac.uk/announcements> or send an email to license@ebi-sib.ch).
DR EMBL: AF135658; AAC12666.1; -.
DR Genbank: HGNC:17151; ORC6L.
KW DNA replication; Nuclear protein; DNA-binding.
SQ SEQUENCE 252 AA. 28.0% MW. 7884302705145FE CFC64;
Query Match 100.0% Score 28, Feb 1, Local 252;
Best Local Similarity 100.0%, Pct. No. 35;
Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 QDYEE 5
EL 230 QDYEE 234
RESULT 2
ORC6_MOUSE
ID ORC6_MOUSE STANDARD: PRT: 262 AA.
AC Q9W0J8;
UI 16 OCT-2001 (Rel. 40, Created)
DI 16 OCT-2001 (Rel. 40, Last sequence update)

15 JUN 2002 (Rel. 41, Last annotation update)
 ORIGIN: recognition complex subunit 6.
 ORC6L OR ORC6.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 Dean F.B., O'Donnell M.;
 "cDNA cloning of a homolog for Saccharomyces cerevisiae ORC6 from Mus
 musculus";
 BL Submitted (MAR-1999) to the EMBL/GenBank/DBI databases
 -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
 ATP DEPENDENT MANNER (BY SIMILARITY).
 -1- SIMILIT: ORC IS COMPOSED OF SIX SUBUNITS (BY SIMILARITY)
 -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 -1- SIMILARITY: BELONGS TO THE ORC6 FAMILY.

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 or send an email to license@isb.sib.ch).

 EMBL: AF199659; AAC2667.1;
 MD: M61:1929285; orc6L.
 DNA replication; Nuclear protein; DNA-binding.
 KW SEQUENCE: 262 AA; 2918 MW; F8027D9C87B16C CRC64.

 Query Match: 100.0%; Score 28; DB 1; Length 262;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 QOVER 5
 DQ 240 QOVER 244

 RESULT 1
 PAHX HUMAN
 ID PAHX HUMAN STANDARD; PPT: 338 AA.
 A: 014832;
 DT 15 JUL 1999 (Rel. 48, Created)
 DT 15 JUL 1999 (Rel. 48, Last sequence update)
 DT 15 JUN 2002 (Rel. 41, Last annotation update)
 DE Phytanoyl-CoA dioxygenase, peroxisomal precursor (pPhy) (phytanoyl acid oxidase).
 DE (phytanoyl-CoA alpha-hydroxylase) (phy) (phytanoyl acid oxidase).
 GN PHYH OR PAHX.
 OS Homo sapiens (Human)
 EC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 EC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 EC NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A., AND VARIANT PEPIDM TPP-275.
 RX MEDLINE-97467730; PubMed-9326939;
 RA Mahalik S.J., Murrell J.C., Kim D., Sachsteder K.A., Watkins P.A.,
 RA Gould S.J.;
 RA "Identification of PAHX, a Refsum disease gene";
 RA Nat. Genet. 17:185-189(1997).
 [2]
 SEQUENCE FROM N.A. AND VARIANT PEPIDM HIS-269
 RX MEDLINE-97467731; PubMed-9426940;
 RA Jansen G.A., Ofman K., Ferdinandusse S., Willems A.O.,
 RA Skjeldal O.H., Stokke O., Jakobs C., Hesley G.T.N., Waich J.E.,
 RA Wanders K.J.A.;
 RA "Refsum disease is caused by mutations in the phytanoyl-CoA
 hydroxylase gene";

Nat. Genet. 17:190-193(1997).
 [3]
 SEQUENCE FROM N.A.
 RC TISSUE: Leukemia;
 MEDLINE-95162545; PubMed-10051602;
 RA Chambrud B., Radanyi C., Camonis J.H., Rajkowski K., Schumacher M.,
 RA Baulieu E.-E.;
 RA "Immunophilins, refsum disease, and lupus nephritis: the peroxisomal
 enzyme phytanoyl-CoA alpha-hydroxylase is a new FKBP-associated
 protein";
 RT Proc. Natl. Acad. Sci. U.S.A. 96:2104-2109(1999).
 [4]
 SEQUENCE FROM N.A., AND VARIANT PEPIDM ALA-192 INS.
 RX PubMed-10767344;
 RA Jansen G.A., Roghooft E.M., Ferdinandusse S., Waterham H.K.,
 RA Ofman K., Jakobs C., Skjeldal O.H., Wanders K.J.A.;
 RA "Human phytanoyl-CoA hydroxylase: resolution of the gene structure and
 the molecular basis of Refsum's disease";
 RT Hum. Mol. Genet. 9:1195-1200(2000).
 PL 1- FUNCTION: CONVERTS PHYTANOL-COA TO 2-HYDROXYPHYTANOL-COA.
 CC 1- CATALYTIC ACTIVITY: Phytanoyl-CoA + 2-oxoglutarate + O(2) -> 2-
 hydroxyphytanoyl-CoA + succinate + CO(2).
 CC 1- COFACTOR: Iron and ascorbate.
 CC 1- PATHWAY: Alpha-oxidation of 3-methyl branched fatty acids
 (phytanic acid); second step.
 CC 1- SUBUNIT: INTERACTS SPECIFICALLY WITH THE IMMUNOPHILIN FKBP52.
 CC 1- SUBCELLULAR LOCATION: Peroxisomal
 CC 1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, AND T-CELLS, BUT
 NOT IN SPLEEN, BRAIN, HEART, LUNG, AND SKELETAL MUSCLE.
 CC 1- DISEASE: DEFECTS IN PHYH ARE THE CAUSE OF REFSUM DISEASE. AN
 AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED CLINICALLY BY A TETRAD
 OF ABNORMALITIES: RETINITIS PIGMENTOSA, PERIPHERAL NEUROPATHY,
 CEREBELLAR ATAXIA, AND ELEVATED PROTEIN LEVELS IN THE
 CEREBROSPINAL FLUID (CSF). PATIENTS EXHIBIT ACCUMULATION OF THE
 BRANCHED-CHAIN FATTY ACID, PHYANIC ACID, IN BLOOD AND TISSUES.
 CC LESS CONSTANT FEATURES ARE NERVE DEAFNESS, ANOSMIA, SKELETAL
 ABNORMALITIES, ICHTHYOSIS, CATARACTS AND CARDIAC IMPAIRMENT.
 CC MANIFESTATIONS OF THE DISEASE APPEAR IN THE SECOND OR THIRD DECADE
 OF LIFE.

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 or send an email to license@isb.sib.ch).

 EMBL: AF023462; AAB81834.1;
 EMBL: AF112977; AAC20602.1;
 EMBL: AF242386; AAF74123.1;
 EMBL: AF242379; AAF74123.1; JOINED.
 EMBL: AF242380; AAF74123.1; JOINED.
 EMBL: AF242381; AAF74123.1; JOINED.
 EMBL: AF242382; AAF74123.1; JOINED.
 EMBL: AF242383; AAF74123.1; JOINED.
 EMBL: AF242384; AAF74123.1; JOINED.
 EMBL: AF242385; AAF74123.1; JOINED.
 Genew: HGNC:8940; PHVH.
 MIM: 602026;
 MIM: 601996;
 MIM: 265500;
 KW Oxidoreductase, Peroxisome; Vitamin C, Iron; Transit peptide;
 Disease mutation.
 FT TRANSIT 1 30 MICROBODY (BY SIMILARITY).
 FT CHAIN 31 338 PHYTANOL-COA DIOXYGENASE.
 FT VARIANT 192 192 A -> AA (IN REFSUM).
 FT VARIANT 269 269 R -> H (IN REFSUM).
 FT VARIANT 275 275 R -> W (IN REFSUM).
 FT VARIANT 275 275 R -> W (IN REFSUM).
 FT SEQUENCE 338 AA; 38538 MW; FBF9639E7C79A6B0 CRC64;
 FT SEQUENCE 338 AA; 38538 MW; FBF9639E7C79A6B0 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QDYE 5
 DB 247 QDYE 241

RESULT 4

SYN_PYPAB STANDARD: PPT: 385 AA
 AC Q9J014: 15-JUN-2002 (Rel. 41, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last sequence update)
 DE TRYPTOPHANYL-TRNA synthetase (EC 6.1.1.2) (Tryptophan-TRNA ligase)
 GN TPFS OR PAB111.
 OS Pyrococcus abyssi.
 CC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcales.
 CC Pyrococcus.
 CC Pyrococcus.
 CC NCBI_TaxID-29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GE5 / Orsay.
 RA Helig R.;
 RT "Pyrococcus abyssi genome sequence. Insights into archaeal chromosome structure and evolution."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBI databases
 CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + TRNA(trp) -> AMP + diphosphate; L-tryptophanyl-TRNA(trp).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC PMBL: AJ248288; CA650601.1;
 DR InterPro: IPR002306; Trp-TRNA-synt_lb.
 DR InterPro: IPR002305; Trp-TRNA-synt_lb.
 DR InterPro: IPR001412; TRNA-synt_1.
 DR Pfam: PF00579; TRNA-synt_lb; 1.
 DR PRINTS: PR01019; TRNASYNTHTRP.
 DR TIGRFAMs: TIGR00233; TPFS; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_1; 1.
 KW Aminoacyl-TRNA synthetase, Protein biosynthesis, Ligase; AIP-binding;
 KW Complete proteome.
 FT SITE 82 90 "HIGH" REGION.
 FT SITE 253 257 "KMSKS" REGION.
 FT SITE 385 AA; 45100 MW; 40200014147412 CP064;
 SQ SEQUENCE 385 AA; 45100 MW; 40200014147412 CP064;

Query Match 100.0%; Score 28; DB 1; Length 385;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QDYE 5
 DB 66 QDYE 70

RESULT 5

SYN_CHLPN STANDARD: PPT: 505 AA.
 AC Q9J014: 30-MAY-2000 (Rel. 39, Last sequence update)
 DI 30-MAY-2000 (Rel. 39, Last sequence update)

DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-TRNA synthetase (EC 6.1.1.17) (glutamate--TRNA ligase) (GluRS).
 CC 251X Gc J190560 OR G10190.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiophila.
 CC NCBI_TaxID-83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CWI029;
 RC MEDLINE-99200006; PubMed-10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Greenwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis." Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AR39;
 RC MEDLINE-20150255; PubMed-10684935;
 RA Read T.D., Bruchan K.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback L., Perry K., Bass S., Lindet K., Weidman J., Khouri H., Craven H., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39." Nucleic Acids Res. 28:1347-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RC MEDLINE-20330349; PubMed-10811462;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Tsuchi K., Shiba T., Ishii K., Hattori M., Kohara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWI029 from USA." Nucleic Acids Res. 28:2311-2314(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 CC -!- CATALYTIC ACTIVITY: AIP + L-glutamate -> AMP + diphosphate + L-glutamyl-TRNA(Glu).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC PMBL: AF001740; A018700.1;
 DR EMBL: AF002140; AAF38063.1;
 DR EMBL: AP002547; HAA98766.1;
 DR HSSP: P27000; 1GLN
 DR TIGR: CP0190;
 DR InterPro: IPR004527; GluX-bact.
 DR InterPro: IPR000924; Glu-TRNA-synt_lb.
 DR InterPro: IPR001412; TRNA-synt_1.
 DR Pfam: PF00749; TRNA-synt_lb; 1.
 DR PRINTS: PR00387; TRNASYNTHGLU.
 DR TIGRFAMs: TIGR00464; GluX-bact; 1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE_1; 1.
 KW Aminoacyl-TRNA synthetase, Protein biosynthesis, Ligase; AIP-binding;
 KW Complete proteome.
 FT SITE 12 22 "HIGH" REGION.
 FT SITE 253 257 "KMSKS" REGION.
 FT BINDING 256 256 ATP (BY SIMILARITY).
 SQ SEQUENCE 505 AA; 58205 MW; 91858007031E6695 CP064;

Query Match 100.0%; Score 28; DB 1; Length 505;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 QYEE 5

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DB 54 QYEE 58

RESULT 6

EZRI_HUMAN STANDARD; PRT; 580 AA.
 AC P15111; P23714; Q9NSJ4;
 DT 01-JUL-1993 (Rel. 26, created)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DE 16-OCT-2001 (Rel. 40, last annotation update)
 DE Ezrin (p81) (Cyto villin) (Villin 2).
 GN VIL2.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID:9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE: Brain;
 RA Bergson C.M., Zhao H., Saijoh K., Doman E.S., Nestler E.J.;
 RT "Ezrin and osteonectin, two proteins associated with cell shape and
 growth, are enriched in the locus coeruleus.";
 RL Mol. Cell. Neurosci. 4:64-74(1993).
 RN [2]
 RP SEQUENCE OF 1-15 AND 126-140.
 RC TISSUE: Kidney;
 RA Galat A., Gerbod M.C., Hout F., Riviere S.;
 RT "Proteins and their amino acid compositions: uniqueness, variability,
 and applications.";
 RL Arch. Biochem. Biophys. 330:229-237(1996).
 CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
 CC -1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
 CC (CYTOPLASMIC SIDE).
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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EMBL: M98498; AAA30510.1;
 InterPro: IPR000290; Band_4.1.
 Pfam: PF00373; Band_4.1;
 Pfam: PF00769; ERM; 1;
 PRINTS: PR00935; HAND1.
 SMART: SM00295; H41; 1;
 PROSITE: PS00660; BAND_4.1; 1;
 PROSITE: PS00661; BAND_4.1; 1;
 PROSITE: PS00057; BAND_4.1; 1;
 KW Structural protein; Cytoskeleton; Phosphorylation.
 FI INIT_MET 0 0
 FI DOMAIN 57 224 BAND: 4.1-LIKE.
 FT M0_RES 145 145 PHOSPHORYLATION (BY PDGFR)
 FT M0_RES 353 353 (BY SIMILARITY).
 FT M0_RES 353 353 PHOSPHORYLATION (BY PDGFR)
 FT M0_RES 353 353 (BY SIMILARITY).
 SEQUENCE 580 AA; 68629 MW; ECD063E5C200FAA3 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 580;

Best Local Similarity 100.0%; Pred No. 88;

Matches %; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5

|||||

DB 351 QYEE 355

RESULT 7

EZRI_HUMAN STANDARD; PRT; 585 AA.
 AC P15111; P23714; Q9NSJ4;
 DT 01-APR-1990 (Rel. 14, created)
 DT 01-NOV-1991 (Rel. 20, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Ezrin (p81) (Cyto villin) (Villin 2).
 GN VIL2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC MEDLINE:90076135; PubMed:2591371;
 RA Gould K.L., Bretscher A., Esch F.S., Hunter T.;
 RT "cDNA cloning and sequencing of the protein tyrosine kinase
 substrate, ezrin, reveals homology to band 4.1.";
 RL EMBO J. 8:4133-4142(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RA Turunen O., Winqvist R., Pakkanen R., Grzeschik K.-H., Wahlstrom T.,
 RA Vaheri A.;
 RT "Cyto villin, a microvillar Mr 75,000 protein, cDNA sequence,
 prokaryotic expression, and chromosomal localization.";
 RL J. Biol. Chem. 264:16727-16732(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RA Ottenwälder H., Obermaier B., Mewes H.-W., Weill R., Wiemann S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 171-179 AND 342-349.
 RA MEDLINE:96311348; PubMed:8713105;
 RA Egerlon M., Moritz R.L., Drucker B., Kelso A., Simpson R.J.;
 RT "Identification of the 70kD heat shock cognate protein (hsc70) and
 alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
 lymphocytes.";
 RL Biochem. Biophys. Res. Commun. 224:666-674(1996).
 RN [5]
 RP PHOSPHORYLATION BY PDGFR.
 RA MEDLINE:92406868; PubMed:1383070;
 RA Krieg J., Hunter T.;
 RT "Identification of the two major epidermal growth factor-induced
 tyrosine phosphorylation sites in the microvillar core protein
 ezrin.";
 RL J. Biol. Chem. 267:19258-19264(1992).
 RN [6]
 RP PHOSPHORYLATION.
 RA MEDLINE:92388649; PubMed:1381389;
 RA Egerlon M., Burgess W.H., Chen D., Drucker B.J., Bretscher A.,
 RA Samelson L.E.;
 RT "Identification of ezrin as an 81 kDa tyrosine phosphorylated protein
 in T cells.";
 RL J. Immunol. 149:1847-1852(1992).
 CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
 CC STRUCTURES TO THE PLASMA MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
 CC (CYTOPLASMIC SIDE).
 CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
 CC EPITHELIAL CELLS.
 CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
 CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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EMBL: AL096809; CAB46772.1; -
 HSSP: P00962; 1GTR.
 InterPro: IPR004514; GlnS.
 InterPro: IPR000924; Gln_rRNA-synt_1c.
 InterPro: IPR001412; rRNA-synt_1.
 Pfam: PF00749; rRNA-synt_1c; 1.
 PRINTS: PR00987; TRNASYNTHGL.
 TIGRFAMs: TIGR00440; glnS; 1.
 PROSITE: PS00178; AA_rRNA_LIGASE; 1.
 AMBIOACYL-rRNA synthetase; protein biosynthesis; ligase, ATP-binding.
 SITE 269 279 "HIGH" REGION.
 SITE 502 506 "KMSKS" REGION.
 BINDING 505 505 ATP (BY SIMILARITY).
 SEQUENCE 811 AA; 92072 MW; AA346369990F94CE CR664;

Query Match 100.0%; Score 28; DB 1; Length 811;

Best local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0.

Matches 5; Conservative 0;

QY 1 QYEE 5

11111

DB 3 QYEE 7

RESULT 10

DD20_HUMAN STANDARD: PRI: 824 AA.
 Q9UHI6; Q9UHI6; GONVYD; GONVYD; Gonpes; Q96F72.
 16-OCT-2001 (Rel. 40, created)
 16-OCT-2001 (Rel. 40, last sequence update)
 15 JUN 2002 (Rel. 42, last annotation update)
 Probable ATP-dependent RNA helicase DDX26 (DEAF-box protein 26) (DEAF-box protein DP 103) (Component of goms 3) (Gom13).
 DDX20 OR GEMIN3 OR DP103.
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A. AND MASS SPECTROMETRY.
 MEDLINE=20069784; PubMed=1040133;
 Charroux B., Pellizzoni I., Parkinson P.A., Shewchenko A., Mann M., Dreyfuss G.
 "Gemini: a novel DEAF box protein that interacts with SMN, the spinal muscular atrophy gene product, and a component of goms.";
 J. Cell Biol. 147:1181-1194(1999).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=9315855; PubMed=10483418;
 Grundhoff A.T., Kromer E., Tureci O., Glieden A., Gindoff C., Alz J., Mueller-Lantzsch N., Schubach W.H., Grasser F.A.;
 "Characterization of Nip13, a novel DEAF box protein that binds to the Epstein-Barr virus nuclear proteins EBNA2 and EBNA3C.";
 J. Biol. Chem. 274:19136-19144(1999).
 [3]
 SEQUENCE FROM N.A.
 Coville G.;
 Submitted (SEP 1999) to the EMBL/GenBank/DDBJ databases
 [4]
 SEQUENCE FROM N.A.
 Isozaki T., Ito T., Hayashi K., Sudiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Suqano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahata K., Masuko Y., Kanchohri K.;
 "NED0 human cDNA sequencing project.";
 Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

[5]
 SEQUENCE FROM N.A.
 TISSUE-Placenta;
 Strausberg R.;
 Submitted (JUL 2001) to the EMBL/GenBank/DDBJ databases.
 [6]
 SEQUENCE OF 393-824 FROM N.A.
 TISSUE-Testis;
 Ansoerg W., Witkner U., Mowes H.-W., Gassenhuber J., Wiemann S.;
 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 -1- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA SPLICING IN THE NUCLEUS.
 -1- SUBUNIT FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEURON PROTEIN (SMN), GEMIN2 AND GEMIN4. INTERACTS DIRECTLY WITH SMN, SM H, SM D2 AND SM D3. INTERACTS WITH ERV ERNA2 AND ERNA3C.
 -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR. LOCALIZED IN SUBNUCLEAR STRUCTURES NEXT TO COILED BODIES, CALLED GEMS, WHICH ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPs.
 -1- TISSUE SPECIFICITY: UBQUITOUS.
 -1- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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EMBL: AF17063; AF14544.1; -
 EMBL: AF106019; AAD42744.1; -
 EMBL: AL049557; CAH55686.2; -
 EMBL: AK001506; BAA91727.1; -
 EMBL: BC011556; AAL1556.1; -
 EMBL: AL133598; CAB63734.1; -
 HSSP: Q58083; 1HVR.
 Genes: HGN:2743; DEX20.
 MIM: 606168; -
 InterPro: IPR001410; DEAF.
 InterPro: IPR000629; DEAF-box.
 InterPro: IPR001650; Helicase_C.
 Pfam: PF00270; DEAF; 1.
 Pfam: PF00271; Helicase_C; 1.
 SMART: SM00487; DEXDC; 1.
 SMART: SM00490; HELIC; 1.
 PROSITE: PS00039; DEAF_ATP_HELICASE; 1.
 Helicase; ATP-binding, DNA-binding, Nuclear protein, mRNA processing;
 Spliceosome.
 NP_BIND 106 113 ATP (POTENTIAL).
 SITE 211 214 DEAD BOX.
 DOMAIN 456 548 SMN INTERACTING.
 FT CONFLICT 5 5 F -> V (IN REF. 2).
 FT CONFLICT 279 279 Y -> C (IN REF. 4).
 FT CONFLICT 393 403 YMERIGRAGR -> MYVLESILL (IN REF. 6).
 FT CONFLICT 636 646 1 -> T (IN REF. 5 AND 6).
 FT CONFLICT 639 639 R -> K (IN REF. 1).
 FT CONFLICT 659 659 Y -> H (IN REF. 2).
 FT CONFLICT 676 676 G -> S (IN REF. 1).
 FT CONFLICT 703 703 S -> T (IN REF. 1).
 SQ SEQUENCE 824 AA; 92240 MW; 7672F024BAC0F2 CR664;

Query Match 100.0%; Score 28; DB 1; Length 824;

Best local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5

11111

DB 771 QYEE 775

RESULT 11

DD20_MOUSE

ID D020_MOUSE STANDARD: PRT: 825 AA.
 AC Q9JY4: Q9JY4; (Rel. 40, Created)
 DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ATP-dependent PNA helicase DDX20 (DEAD-box protein DP103) (Component of gems 3) (Gemin3) (Regulator of steroidogenic factor-1) (POSF-1)
 DE box protein DP103 (Component of gems 3) (Gemin3) (Regulator of steroidogenic factor-1) (POSF-1)
 GN DDX20 OR GEMIN3 OR DP103.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20331537; PubMed=10757334;
 RA Campbell L., Hunter K.M., Mohaghegh P., Tinsley J.M., Brasch M.A., Davies K.E.;
 RT "Direct interaction of Smn with dp103, a putative RNA helicase, a role for Smn in transcription regulation?";
 RT Hum. Mol. Genet. 9:1093-1100(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE-Testis;
 PA C. O. Mueller, I. F. Perez, S. Yan X., Crawford P.A., Szybski Y.;
 RT "The DEAD box protein DDX20 is a regulator of steroidogenic factor-1";
 RT J. Biol. Chem. 275:11093-11098(2000).
 RN [3]
 RP Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases
 CC -!- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPINCEOSOMAL SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PPE-MPNA SPLICING IN THE NUCLEUS.
 CC -!- SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR NEURON PROTEIN (SMN), GEMIN2 AND GEMIN3. INTERACTS DIRECTLY WITH SMN, SM B, SM D2 AND SM D3.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR, LOCALIZED IN SUBNUCLEAR STRUCTURES NEXT TO C-TERMINUS, CALLED GEMS, WHICH ARE HIGHLY ENRICHED TO THE DEAD BOX HELICASE FAMILY.
 CC -!- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
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 DR EMBL: AJ250027; CAB86201.1; -;
 DR EMBL: AF220454; AAF76381.1; -;
 DR HSSP: Q580A3; 1HV8
 DR MGD: MGI:1858415; DDX20.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR0000829; DEAD_BOX.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR SMART: SM00487; DEKDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 DR SMART: PS00049; DEAD_ATP_HELICASE; 1.
 KW Helicase. ATP-binding, DNA-binding, Nuclear protein, mRNA processing.
 KW Spliceosome.
 FT NP_BIND 107 114 ATP (POTENTIAL).
 FT SITE 212 215 DEAD BOX.
 FT CONFLICT 5 5 A -> T (IN REF. 2).
 FT CONFLICT 9 9 P -> R (IN REF. 2).
 FT CONFLICT 226 226 E -> G (IN REF. 2).
 FT CONFLICT 468 468 V -> I (IN REF. 2).
 SQ SEQUENCE 825 AA; 91719 MW; F6D06E2E8A7D2D CRC64;

Query Match 100.0% Score 28, DR 1, Length 825,

Best Local Similarity 100.0%, Prod. No. 13032,

Matches 5; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYEE 5
 DB 772 QYEE 776
 RESULT 12
 IKAP_HUMAN
 ID IKAP_HUMAN STANDARD: PRT: 1332 AA.
 AC Q95163; Q95163; Q95163;
 DI 16-OCT-2001 (Rel. 40, Created)
 DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE IkappaB kinase complex-associated protein (IKK complex-associated protein) (p150).
 DE protein (p150).
 GN IKKAP OR IKAP.
 GN IKKAP_HUMAN (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC TISSUE=Cervical carcinoma;
 RA Cohen L., Henzel W.J., Baeuerle P.A.;
 RX MEDLINE=98421679; PubMed=9751059;
 RT "IKAP is a scaffolding protein of the IkappaB kinase complex";
 RT Nature 395:292-296(1998).
 RN [2]
 RP SEQUENCE FROM N.A. AND VARIANT PD PRO-696.
 RX MEDLINE=21095531; PubMed=11179008.
 PA Slagterhans S.A., Blumenthal A., Gill S.P., Leyue M., Mull J., Slagterhans S.A., Blumenthal A., Chadwick B.P., Idelson M., Reznik L., Rodriguez M.P., Makalowska I., Brownstein M.J., Krappmann D., Scheldereit C., Maayan C., Axelrod P.B., Gussella J.P.;
 RA "Tissue specific expression of a splicing mutation in the IKKAP gene causes familial dysautonomia";
 RT Am. J. Hum. Genet. 68:598-605(2001).
 PL [3]
 RP SEQUENCE OF 961-1332 FROM N.A.
 RC TISSUE=Brain;
 RA Wambutt R., Holtkamp B., Mowes H.W., Gassenhuber J., Wichmann S.;
 RX Submitt (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP VARIANT PD PRO-696, AND EFFECT ON PHOSPHORYLATION.
 RX MEDLINE=21095531; PubMed=11179008.
 RA Anderson S., Coll M., Daly L.W., Kichula E.A., Rork M.J., Volpi S.A., Ekstein J., Rubin B.Y.;
 RT "Familial dysautonomia is caused by mutations of the IKAP gene";
 RT Am. J. Hum. Genet. 68:753-758(2001).
 CC -!- FUNCTION: MAY ACT AS A SCAFFOLD PROTEIN THAT MAY ASSEMBLE ACTIVE IKK-MAP3K14 COMPLEXES (IKKA, IKKB AND MAP3K14/NIK).
 CC -!- SUBUNIT: INTERACTS PREFERENTIALLY WITH MAP3K14/NIK FOLLOWED BY IKK-ALPHA AND IKK-BETA.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: PHOSPHORYLATED.
 CC -!- DISEASE: DEFECTS IN IKKAP ARE THE CAUSE OF FAMILIAL DYSAUTONOMIA (FD). ALSO KNOWN AS RILEY-DAY SYNDROME OR HEREDITARY SENSORY AND AUTONOMIC NEUROPATHY TYPE III. THIS AUTOSOMAL RECESSIVE DISORDER IS DUE TO THE POOR DEVELOPMENT AND SURVIVAL, AND PROGRESSIVE DEGENERATION OF THE SENSORY, SYMPATHETIC AND PARASYMPATHETIC NERVOUS SYSTEMS. INDIVIDUALS ARE AFFECTED WITH A VARIETY OF SYMPTOMS SUCH AS DECREASED SENSITIVITY TO PAIN AND TEMPERATURE, CARDIOVASCULAR INSTABILITY, RECURRENT PNEUMONIAS, VOMITING CRISES, AND GASPOUNTS. FAMILIAL DYSAUTONOMIA IS PRIMARILY CONFINED TO INDIVIDUALS OF ASHKENAZI JEWISH DESCENT, WITH AN INCIDENCE OF 1/4600 LIVE BIRTHS.
 CC -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 1286.
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EMBL: AF044195; AAC64258.1; -
EMBL: AF154419; AAC43369.1; -
EMBL: AF049945; CAB43219.1; ALL_FRAME.
GenBank: HGNC:5959; IKHKAP.
MIN: 603722; -
MIN: 224900; -
Phosphorylation: Disease mutation.
VARIANT 696 696
R -> P (IN PD; MILD PHENOTYPE;
PHOSPHORYLATION IS REDUCED).
/FLN-VAR_011327
K -> W (IN REF. 2).
K -> E (IN REF. 3).
P -> L (IN REF. 2).
C -> G (IN REF. 3).
S -> C (IN REF. 1).
P -> L (IN REF. 3).
I -> V (IN REF. 3).
V59191.W: 3FD65FA8554DA523_CRG64.
SEQUENCE 1342 AA: 59191

```

```

Query Match      100.0%   Score 28;   DB 1;   Length 1332;
Best Local Similarity 100.0%;   Pred. No. 226962;
Matches 5;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY          1 QYEE 5
            |||||
IB         1074 QYEE 1078

RESULT 13
YYO/O..METJA        STANDARD;       PPT;       82 AA.
AC      Q60374;
D1      01-NOV-1997 (Rel. 35, Created)
D1      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein MJ0070.
GN      MJ0070.
OS      Methanococcus jannaschii.
SS      Archaea; Euryarchaeota; Methanococci; Methanococcales;
SC      Methanocaldococcaceae; Methanocaldococcus.

```

SEQUENCE FROM N.A.
STRAIN JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96347999; PubMed-BE080087;
Bolt C.J., White O., Olson G.J., Zhou L., Fleischmann R.D.,
Sartori C.G., Blake J.A., Karlovich J.M., Clayton R.A., Cocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.L.,
Overbeek R., Kirkness E.F., Weisskopf K.G., Merrick J.M., Glocke A.,
Scott J.L., Goodenow N.S., Weidman J.F., Fudman T.L., Nguyen P.,
Uffetback L.R., Kelley J.M., Petersen J.F., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.G., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, *Methanocaldococcus*
jannaschii,"
Science 273:1058-1073(1996).

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EMBL; U67464; AAB98053.1; -
 TIGR; MJ0070; -
 Hypothetical protein; Complete proteome.
 DOMAIN 46 58 GLU-RICH.
 SEQUENCE R2 AA; 9,007 MW; 298236477835550P C9664;

```

Query Match      89.38; Score 25; DB 1; Length 130;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
07 1 COVER 5

```


Db 56 QDYEQ 60

RESULT 15

CAL2_RAT
ID CAL2_RAT STANDARD: PRT: 134 AA.
AC P10093;
DI 01-MAR-1989 (Rel. 10, Created)
DI 01-MAR-1989 (Rel. 10, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Calcitonin gene-related peptide-II precursor (CGRP-II) (Beta-type
DE CGRP).
GN CALCB.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85300490; PubMed=2994212;
FA Andra S.G., Ariza J.L., Jeff S.E., Swanson L.W., Evans R.M.,
RA Rosenfeld M.G.;
RT "Expression in brain of a messenger RNA encoding a novel neuropeptide
RT homologous to calcitonin gene-related peptide.";
RL Science 229:1094-1097(1985).
CC -!- FUNCTION: CGRP induces vasodilatation. It dilates a variety of
CC vessels including the coronary, cerebral and systemic vasculature.
CC Its abundance in the CNS also points toward a neurotransmitter or
CC neuromodulator role.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M11596; AAA0850.1; -;
DR PIR: A44173; A44173.
DR InterPro: IPR001693; Calcitonin-like.
DR InterPro: IPR002163; Calcitonin_R.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
KW cleavage on pair of basic residues; Amidation; Hormone; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT PROPEP 27 86 BY SIMILARITY.
FT PEPTIDE 89 125 CALCITONIN GENE-RELATED PEPTIDE II.
FT PROPEP 131 134 BY SIMILARITY.
FT DISULFID 90 95 BY SIMILARITY.
FT MOD_RES 125 125 AMIDATION (G-126 PROVIDE AMIDE GROUP) (BY
FT SIMILARITY).
SQ SEQUENCE 134 AA: 14965 MW: 48938 CRC64:
Query Match 89.3% Score 25; DB 1; Length 134;
Best Local Similarity 80.0%; Pred. No. 79;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 QDYEQ 5

Db 56 QDYEQ 60

Search completed: January 16, 2003, 16:51:17
Job time : 8.28571 secs

